AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 12, line 13 to read:

The term "sequence identity" herein used refers to the identity and homology between two proteins. The "sequence identity" is determined by comparing two sequences aligned optimally over the regions corresponding to the sequences to be compared. In this context, the both proteins to be compared may have addition or deletion (e.g., "gap") in their sequences for optimum alignment. Such sequence identity can be calculated by preparing alignment using, for example, Vector NTI, ClustalW algorithm (Nucleic Acid Res., 22 (22): 4673-4680(1994)). The sequence identity can be determined using software for sequence analysis, specifically, Vector NTI or GENETYX-MAC, or a sequencing tool provided by a public database. ~~Such a public database is commonly available at Web site (http://www.ddbj.nig.ac.jp).~~

Please amend the paragraph beginning on page 17, line 3 to read:

Recently, it has become possible to search peptide sequences expected to be capable of binding to HLA antigens via the internet using BIMAS software~~; NIH (http://bimas.dcrt.nih.gov/molbio/hla_bind/)~~.

Please amend the paragraph beginning on page 23, line 7 to read:

As mentioned above, motifs for antigen peptides that bind to an HLA and presented are known in regard to certain HLA types, such as HLA-A1, -A0201, -A0204, -A0205, -A0206, -A0207, -A11, -A24, -A31, -A6801, -B7, -B8, -B2705, -B37, -Cw0401 and -Cw0602. Further, it is possible to search for peptide sequences that are expected to be able to bind to HLA antigen via internet ~~(http: // bimas.dcrt.nih.gov / molbio / hla_bind /)~~. Thus, one can prepare the variant peptides above on the basis of these motifs and the like.

Please amend the paragraph beginning on page 23, line 15 to read:

For example, as hereinbefore described, motifs of antigen peptides capable of binding to HLA-A24 and being presented are known that, in the 8 - 11 amino acid peptide, the amino acid at position 2 is tyrosine, phenylalanine, methionine or tryptophan, and the C terminal amino acid

is phenylalanine, leucine, isoleucine, tryptophan or methionine (J. Immunol., 152: p3913, 1994; Immunogenetics, 41: p178, 1995; J. Immunol., 155: p4307, 1994). As for HLA-A2, the motifs listed in Table 1 above are known. Furthermore, there are published via internet certain peptide sequences that are expected to be able to bind to HLA antigen ~~(http://bimas.dcrt.nih.gov/molbio/hla_bind/)~~. Accordingly, amino acids having a similar characteristic to those available for the motif above are acceptable. Thus, the present invention includes variant peptides comprising an amino acid sequence wherein an amino acid(s) at position(s) available for substitution in light of motif (in the case of HLA-A24 and HLA-A2, position 2 and C-terminus) is substituted by other amino acid, preferably, an amino acid expected to have binding activity as a result of internet search, and having an activity of binding to HLA and being recognized by CTLs.

Please amend the paragraph beginning on page 31, line 30 to read:

The term "sequence identity" herein used refers to the identity and homology between two polynucleotides. The "sequence identity" is determined by comparing two sequences aligned optimally over the regions corresponding to the sequences to be compared. In this context, the both polynucleotides to be compared may have addition or deletion (e.g., "gap") in their sequences for optimum alignment. Such sequence identity can be calculated by preparing alignment using, for example, Vector NTI, ClustalW algorithm (Nucleic Acid Res., 22 (22): 4673-4680(1994)). The sequence identity can be determined using software for sequence analysis, specifically, Vector NTI or GENETYX-MAC, or a sequencing tool provided by a public database. ~~Such a public database is commonly available at Web site (http://www.ddbj.nig.ac.jp).~~

Please amend the paragraph beginning on page 52, line 6 to read:

For example, the tumor marker of the present invention can be designed on the basis of the base sequence shown in SEQ ID NO: 1 or 3 by means of primer 3 ~~(HYPERLINK http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi)~~ or a vector NTI (Infomax). Specifically, a candidate sequence for primer or probe, or a sequence at least comprising said

sequence as a partial sequence can be used as a primer or probe, which candidate sequence is obtainable by subjecting the base sequence of the gene of the present invention to primer 3 or vector NTI software. Example of such a tumor marker of the present invention includes a primer shown in SEQ ID NO: 4 or 5.